

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: CEDARS-SINAI MEDICAL CENTER
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Campbell & Flores LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Ramos, Robert T.
 - (B) REGISTRATION NUMBER: 37,915
 - (C) REFERENCE/DOCKET NUMBER: FP CE 2563
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGTAGCAA CGGAAACGGC GCGGGCGCGT TTCGGCCCCG CTCCCCGCGG CTCCTTGATC	60
TCGGCGGGCC TCCCCGCCCC TTCGTCTGTC TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC	120
CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TCGTCCCCG CCGCGTTCCG	180

36T60" 86T6680

GCGTCTCCTT GCGCGCCCCG GCTCCCGGCT GTCCCCGCCC GCGGTGCGAG CCGGTGTATG 240
 GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300
 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360
 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT 420
 CCGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480
 GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC 516

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG 60
 GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCGCACTTC CGGTAAAGAG TCCCTATCCG 120
 CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCGCGCCCTC CG ATG CGC TCA GCG 174
 Met Arg Ser Ala
 1
 GCC GCA GCT CCT CGG AGT CCC GCG GTG GGC ACC GAG TCT CGC CGC TTC 222
 Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe
 5 10 15 20
 GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG 270
 Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg
 25 30 35
 CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC 318
 Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser
 40 45 50
 GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC 366
 Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser
 55 60 65

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TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC 414
 Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly
 70 75 80

GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT 462
 Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro
 85 90 95 100

CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC 510
 Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala
 105 110 115

CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC 558
 Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser
 120 125 130

CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC 606
 Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro
 135 140 145

CGC CCG GCG TGC GAG CCG GTG TAT GGG CCG CTC ACC ATG TCG CTG AAG 654
 Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys
 150 155 160

CCC CAG CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG 702
 Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 165 170 175 180

CAG CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC 750
 Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg
 185 190 195

AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG 798
 Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser
 200 205 210

CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG 846
 Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser
 215 220 225

GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT 894
 Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly
 230 235 240

CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA 942
 Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly
 245 250 255 260

ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC 990
 Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly
 265 270 275

TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT 1038
 Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val
 280 285 290

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TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT	1086
Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His	
295 300 305	
GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG	1134
Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met	
310 315 320	
GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA	1182
Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys	
325 330 335 340	
GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT	1230
Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala	
345 350 355	
ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC	1278
Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro	
360 365 370	
TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA	1326
Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu	
375 380 385	
AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT	1374
Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn	
390 395 400	
GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG	1422
Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser	
405 410 415 420	
TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG	1470
Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg	
425 430 435	
GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG	1518
Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln	
440 445 450	
TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA	1566
Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu	
455 460 465	
AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC	1614
Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser	
470 475 480	
ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA	1662
Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg	
485 490 495 500	
GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC	1710
Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly	
505 510 515	

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CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA	1758
Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser	
520 525 530	
GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT	1806
Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly	
535 540 545	
GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT	1854
Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser	
550 555 560	
CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT	1902
Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro	
565 570 575 580	
ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT	1950
Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser	
585 590 595	
CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA	1998
His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys	
600 605 610	
CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA	2046
Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg	
615 620 625	
CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT	2094
His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser	
630 635 640	
GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT	2142
Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro	
645 650 655 660	
CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA GTG GTC	2190
Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser Val Val	
665 670 675	
AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC	2238
Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro	
680 685 690	
AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT	2286
Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser	
695 700 705	
CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA	2334
Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro	
710 715 720	
GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC	2382
Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr	
725 730 735 740	

CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC	2430
Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn	
745 750 755	
TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT	2478
Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro	
760 765 770	
AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA	2526
Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu	
775 780 785	
CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG	2574
His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg	
790 795 800	
TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA	2622
Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys	
805 810 815 820	
AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA	2670
Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu	
825 830 835	
CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC	2718
Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn Cys Thr	
840 845 850	
AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT	2766
Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu	
855 860 865	
AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT	2814
Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val	
870 875 880	
CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG	2862
Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu	
885 890 895 900	
AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT	2910
Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn	
905 910 915	
GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT	2958
Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr	
920 925 930	
ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT ATG GTG	3006
Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val	
935 940 945	
GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT TTT GCA	3054
Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys Phe Ala	
950 955 960	

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CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA CCT TTA 3102
Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu
965 970 975 980

TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG ACA TAT 3150
Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr
985 990 995

AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT CAT CAG 3198
Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His His Gln
1000 1005 1010

AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT GCA GCC 3246
Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile Ala Ala
1015 1020 1025

ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG 3294
Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln
1030 1035 1040

TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG 3342
Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln
1045 1050 1055 1060

CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG 3390
His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met
1065 1070 1075

GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT 3438
Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ala Thr
1080 1085 1090

CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA 3486
Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys
1095 1100 1105

TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC 3534
Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser
1110 1115 1120

ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC 3582
Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His
1125 1130 1135 1140

CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG 3630
Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln
1145 1150 1155

CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC 3678
Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His
1160 1165 1170

CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG 3726
His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln
1175 1180 1185

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CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG 3774
 Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met
 1190 1195 1200
 ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA 3822
 Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala
 1205 1210 1215 1220
 CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT 3870
 Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr
 1225 1230 1235
 ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA 3918
 Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser
 1240 1245 1250
 GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG 3966
 Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met
 1255 1260 1265
 ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA 4014
 Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala
 1270 1275 1280
 CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG 4062
 Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr
 1285 1290 1295 1300
 CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAAGGCTGCC 4108
 His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1305 1310
 CTGGAGGAAC CGAAAGGCCA AATTCCCTCC TCCCTTCTAC TGCTTCTACC AACTGGAAGC 4168
 ACAGAAACT AGAATTTTCAT TTATTTTGTT TTTAAAATAT ATATGTTGAT TTCTTGTAAC 4228
 ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGGAAGAT ACTTGGACCG AGTAGAGGCA 4288
 TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC CGCAGGTACC 4348
 CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTSTA ATAACCCTTG AAAGTCATGA 4408
 ACACATCAGC TAGCAAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC TGCTAAAAAA 4468
 AAAAAAAAAA AAA 4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu
 1 5 10 15
 Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln
 20 25 30
 Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly
 35 40 45
 Pro Tyr Pro Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro
 50 55 60
 Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn
 65 70 75 80
 Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly
 85 90 95
 Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala
 100 105 110
 Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly
 115 120 125
 Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala
 130 135 140
 Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr
 145 150 155 160
 Met Ser Leu Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 165 170 175
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala
 180 185 190
 Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala
 195 200 205
 Ala Ala Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr
 210 215 220
 Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly
 225 230 235 240
 Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile
 245 250 255
 Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr
 260 265 270
 Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile
 275 280 285

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Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu
 290 295 300
 Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg
 305 310 315 320
 Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val
 325 330 335
 Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe
 340 345 350
 Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys
 355 360 365
 Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu
 370 375 380
 Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met
 385 390 395 400
 Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser
 405 410 415
 Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu
 420 425 430
 Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu
 435 440 445
 Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg
 450 455 460
 Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg
 465 470 475 480
 Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly
 485 490 495
 Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser
 500 505 510
 Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr
 515 520 525
 Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val
 530 535 540
 Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser
 545 550 555 560
 Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg
 565 570 575

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Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser
 580 585 590
 Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser
 595 600 605
 Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro
 610 615 620
 Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly
 625 630 635 640
 Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu
 645 650 655
 Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp
 660 665 670
 Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg
 675 680 685
 Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro
 690 695 700
 Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala
 705 710 715 720
 Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn
 725 730 735
 Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp
 740 745 750
 Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn
 755 760 765
 Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro
 770 775 780
 Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys
 785 790 795 800
 Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln
 805 810 815
 Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys
 820 825 830
 Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser
 835 840 845
 Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser
 850 855 860

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Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr
 865 870 875 880
 Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp
 885 890 895
 Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr
 900 905 910
 Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro
 915 920 925
 Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser
 930 935 940
 Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro
 945 950 955 960
 Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly
 965 970 975
 Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln
 980 985 990
 Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp
 995 1000 1005
 Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro
 1010 1015 1020
 Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
 1025 1030 1035 1040
 Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
 1045 1050 1055
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
 1060 1065 1070
 Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser
 1075 1080 1085
 Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr
 1090 1095 1100
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
 1105 1110 1115 1120
 Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
 1125 1130 1135
 Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
 1140 1145 1150

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Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
 1155 1160 1165

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
 1170 1175 1180

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
 1185 1190 1195 1200

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser
 1205 1210 1215

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
 1220 1225 1230

Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala
 1235 1240 1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
 1250 1255 1260

Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu
 1265 1270 1275 1280

Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe
 1285 1290 1295

Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 3798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 50..3457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCACGAGGT CCCC GCCCGG CGTGCGAGCC GGTGTATGGG CCGCTCACC ATG TCG
 Met Ser
 1

CTG	AAG	CCG	CAG	CCG	CAG	CCG	CCC	GCG	CCC	GCC	ACT	GGC	CGC	AAG	CCC	103
Leu	Lys	Pro	Gln	Pro	Gln	Pro	Pro	Ala	Pro	Ala	Thr	Gly	Arg	Lys	Pro	
		5					10					15				
GGC	GGC	GGC	CTG	CTC	TCG	TCG	CCC	GGC	GCC	GCG	CCG	GCC	TCG	GCC	GCG	151
Gly	Gly	Gly	Leu	Leu	Ser	Ser	Pro	Gly	Ala	Ala	Pro	Ala	Ser	Ala	Ala	
		20				25					30					
GTG	ACC	TCG	GCT	TCC	GTG	GTG	CCG	GCC	CCG	GCC	GCG	CCG	GTG	GCG	TCT	199
Val	Thr	Ser	Ala	Ser	Val	Val	Pro	Ala	Pro	Ala	Ala	Pro	Val	Ala	Ser	
		35			40					45					50	
TCC	TCG	GCG	GCC	GCG	GGC	GGC	GGG	CGT	CCC	GGC	CTG	GGC	AGA	GGT	CGG	247
Ser	Ser	Ala	Ala	Ala	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	Arg	
				55					60					65		
AAC	AGT	AGC	AAA	GGA	CTG	CCT	CAG	CCT	ACG	ATT	TCT	TTT	GAT	GGA	ATC	295
Asn	Ser	Ser	Lys	Gly	Leu	Pro	Gln	Pro	Thr	Ile	Ser	Phe	Asp	Gly	Ile	
			70					75					80			
TAT	GCA	AAC	GTG	AGG	ATG	GTT	CAT	ATA	CTT	ACG	TCA	GTT	GTT	GGA	TCG	343
Tyr	Ala	Asn	Val	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	Ser	
		85					90					95				
AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAC	GGA	GGC	ATA	TAT	GAA	GGA	GTT	TTT	391
Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	Phe	
		100				105					110					
AAA	ACA	TAC	AGT	CCT	AAG	TGT	GAC	TTG	GTA	CTT	GAT	GCT	GCA	CAT	GAG	439
Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	Glu	
				120					125						130	
AAA	AGT	ACA	GAA	TCC	AGT	TCG	GGG	CCA	AAA	CGT	GAA	GAA	ATA	ATG	GAG	487
Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	Glu	
				135				140						145		
AGT	GTT	TTG	TTC	AAA	TGC	TCA	GAC	TTC	GTT	GTG	GTA	CAG	TTT	AAA	GAT	535
Ser	Val	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	Asp	
			150					155					160			
ACA	GAC	TCC	AGT	TAT	GCA	CGG	AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	CTC	583
Thr	Asp	Ser	Ser	Tyr	Ala	Arg	Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	Leu	
		165					170					175				
AGC	GCA	AAG	GTG	AAT	GGT	GAG	CAC	AAG	GAG	AAG	GAC	CTG	GAG	CCC	TGG	631
Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys	Asp	Leu	Glu	Pro	Trp	
		180				185					190					
GAT	GCA	GGG	GAG	CTC	ACG	GCC	AGC	GAG	GAG	CTG	GAG	CTG	GAG	AAT	GAT	679
Asp	Ala	Gly	Glu	Leu	Thr	Ala	Ser	Glu	Glu	Leu	Glu	Leu	Glu	Asn	Asp	
				200					205							

AAT TAT GGT GTG GTG TCC ACA TAT GAT AGC AGT TTA TCT TCA TAT ACG Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr 230 235 240	775
GTT CCT TTA GAA AGG GAC AAC TCA GAA GAA TTT CTT AAA CGG GAG GCA Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala 245 250 255	823
AGG GCA AAC CAG TTA GCA GAA GAA ATT GAA TCC AGT GCT CAG TAC AAA Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys 260 265 270	871
GCT CGT GTC GCC CTT GAG AAT GAT GAC CGG AGT GAG GAA GAA AAA TAC Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr 275 280 285 290	919
ACA GCA GTC CAG AGA AAC TGC AGT GAC CGG GAG GGG CAT GGC CCC AAC Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly Pro Asn 295 300 305	967
ACT AGG GAC AAT AAA TAT ATT CCT CCT GGA CAA AGA AAC AGA GAA GTC Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg Glu Val 310 315 320	1015
CTA TCC TGG GGA AGT GGG AGA CAG AGC TCA CCA CGG ATG GGC CAG CCT Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly Gln Pro 325 330 335	1063
GGG CCA GGC TCC ATG CCG TCA AGA GCT GCT TCT CAC ACT TCA GAT TTC Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser Asp Phe 340 345 350	1111
AAC CCG AAC GCT GGC TCA GAC CAA AGA GTA GTT AAT GGA GGT GTT CCC Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly Val Pro 355 360 365 370	1159
TGG CCA TCG CCT TGC CCA TCT CAT TCC TCT CGC CCA CCT TCT CGC TAC Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser Arg Tyr 375 380 385	1207
CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CAT ACA CGG Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His Thr Arg 390 395 400	1255
CCG CCC TCC AGG CCC CCC TCG AGG CCA TCC AGA CCC CCG TCT CAC CCC Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser His Pro 405 410 415	1303
TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA CGC ATG Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys Arg Met 420 425 430	1351
TCT TCA GAA GGA CCC CCA AGG ATG TCT CCA AAG GCA CAG CGC CAC CCT Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg His Pro 435 440 445 450	1399

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CGG AAT CAC AGA GTC TCT GCT GGG AGA GGC TCC ATG TCT AGT GGC CTA	1447
Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser Gly Leu	
455 460 465	
GAA TTT GTA TCC CAC AAT CCC CCA AGT GAA GCA GCT GCT CCT CCA GTG	1495
Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro Pro Val	
470 475 480	
GCA AGG ACC AGT CCT GCA GGG GGA ACG TGG TCC TCA GTG GTC AGT GGG	1543
Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val Ser Gly	
485 490 495	
GTT CCA AGG TTA TCT CCC AAA ACT CAC AGA CCC AGG TCT CCC AGG CAG	1591
Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro Arg Gln	
500 505 510	
AGC AGC ATT GGA AAC TCT CCC AGC GGG CCT GTG CTT GCT TCT CCC CAA	1639
Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser Pro Gln	
515 520 525 530	
GCT GGC ATC ATC CCT GCA GAA GCC GTT TCC ATG CCT GTT CCC GCC GCA	1687
Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro Ala Ala	
535 540 545	
TCT CCG ACT CCT GCC AGC CCT GCA TCC AAC AGA GCA CTG ACC CCA TCT	1735
Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr Pro Ser	
550 555 560	
ATT GAG GCA AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC TCT CCT	1783
Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn Ser Pro	
565 570 575	
GCA GGG AGT AAA GAA AAT GTT AAA GCA AGT GAA ACA TCA CCT AGC TTT	1831
Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro Ser Phe	
580 585 590	
TCA AAA GCT GAC AAC AAA GGT ATG TCA CCA GTT GTT TCT GAA CAC AGA	1879
Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu His Arg	
595 600 605 610	
AAA CAG ATT GAT GAC TTA AAG AAG TTT AAG AAT GAT TTT AGG TTA CAG	1927
Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg Leu Gln	
615 620 625	
CCA AGC TCT ACA TCT GAA TCT ATG GAT CAA CTA CTA AGC AAA AAT AGA	1975
Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys Asn Arg	
630 635 640	
GAA GGA GAA AAG TCA CGA GAT TTG ATT AAA GAT AAA ACG GAA GCA AGT	2023
Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Glu Ala Ser	
645 650 655	
GCT AAG GAT AGT TTC ATT GAC AGC AGC AGC AGC AGC AAC TGT ACC	2071
Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Ser Asn Cys Thr	
660 665 670	

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AGT GGC AGC AGC AAG ACC AAC AGC CCT AGC ATC TCC CCT TCC ATG CTT 2119
 Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser Met Leu
 675 680 685 690

AGT AAT GCA GAG CAC AAG AGG GGG CCT GAG GTC ACA TCC CAA GGG GTG 2167
 Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val
 695 700 705

CAG ACT TCC AGC CCA GCC TGC AAA CAA GAG AAG GAT GAC AGA GAA GAG 2215
 Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg Glu Glu
 710 715 720

AAG AAA GAC ACA ACA GAG CAG GTT AGG AAA TCG ACA TTG AAT CCC AAT 2263
 Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn
 725 730 735

GCA AAG GAG TTC AAC CCT CGT TCT TTC TCT CAG CCA AAG CCT TCT ACT 2311
 Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr
 740 745 750

ACC CCA ACG TCA CCT CGG CCT CAA GCA CAA CCC AGC CCA TCT ATG GTG 2359
 Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val
 755 760 765 770

GGT CAT CAG CAG CCA GCT CCA GTG TAC ACT CAG CCT GTG TGC TTC GCA 2407
 Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys Phe Ala
 775 780 785

CCC AAT ATG ATG TAT CCC GTC CCA GTG AGC CCG GGC GTA CAA CCT TTA 2455
 Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu
 790 795 800

TAC CCA ATA CCT ATG ACG CCC ATG CCT GTG AAC CAA GCC AAG ACA TAT 2503
 Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr
 805 810 815

AGA GCA GGT AAA GTA CCA AAT ATG CCC CAA CAG CGA CAA GAC CAA CAT 2551
 Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His
 820 825 830

CAT CAA AGC ACC ATG ATG CAC CCA GCC TCC GCG GCA GGG CCA CCC ATC 2599
 His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile
 835 840 845 850

GTA GCC ACC CCG CCC GCT TAC TCC ACT CAG TAC GTT GCC TAC AGC CCT 2647
 Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro
 855 860 865

CAG CAG TTT CCC AAT CAG CCT TTG GTC CAG CAT GTG CCG CAT TAT CAG 2695
 Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln
 870 875 880

TCT CAG CAT CCT CAT GTG TAC AGT CCT GTC ATA CAA GGT AAT GCC AGG 2743
 Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg
 885 890 895

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ATG ATG GCA CCA CCA GCA CAT GCT CAG CCT GGT TTA GTG TCT TCT TCA	2791
Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser Ser Ser	
900 905 910	
GCT GCT CAG TTC GGG GCT CAC GAG CAG ACG CAC GCC ATG TAT GCA TGT	2839
Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys	
915 920 925 930	
CCC AAA TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC	2887
Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala	
935 940 945	
ATT TCC ACC GGC TCC CTC GCT CAG CAG TAT GCA CAT CCT AAT GCC GCC	2935
Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Ala	
950 955 960	
CTG CAT CCA CAT ACT CCC CAT CCT CAG CCT TCG GCC ACT CCC ACC GGA	2983
Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly	
965 970 975	
CAG CAG CAA AGC CAG CAT GGT GGA AGT CAC CCT GCA CCC AGT CCT GTT	3031
Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val	
980 985 990	
CAG CAC CAT CAG CAC CAG GCT GCC CAG GCT CTT CAT CTG GCC AGT CCA	3079
Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro	
995 1000 1005 1010	
CAG CAG CAG TCG GCC ATT TAT CAT GCG GGG CTG GCA CCA ACA CCA CCT	3127
Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro	
1015 1020 1025	
TCC ATG ACA CCT GCC TCT AAT ACA CAG TCT CCA CAG AGC AGT TTC CCA	3175
Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser Phe Pro	
1030 1035 1040	
GCA GCA CAA CAG ACA GTC TTC ACC ATC CAC CCT TCT CAT GTT CAG CCG	3223
Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro	
1045 1050 1055	
GCA TAC ACC ACC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA	3271
Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala His Val	
1060 1065 1070	
CAG TCA GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG	3319
Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met	
1075 1080 1085 1090	
CTA ATG ACG ACA CAG CCA CCC GGT CCC AAG GCC GCC CTC GCT CAA AGT	3367
Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala Gln Ser	
1095 1100 1105	
GCA CTA CAG CCC ATT CCA GTT TCG ACA ACA GCG CAT TTC CCT TAT ATG	3415
Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met	
1110 1115 1120	

0898498-05498

ACG CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAAGGCTGCC 3464
 Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1125 1130 1135

TTGGAGGAAC CGAAAGGCOA AATCCCTTCT TCCCTTCTCT GCTTCTGCCA ACCGGAAGCA 3524

CAGAAACTA GAACTTCATT GATTTTGTTC TTTAAAAGAT AACTGATTT AACATCTGAT 3584

AGGAATGCTA ACAGCTCACT TGCAGTGGAG GATGTTTTGG ACCGAGTAGA GGCATGTAGG 3644

GACTTGTCGC TGTTCATAA TTCCATGTGC TGTTCAGGG TCCTGCAAGT ACCCAGCTCT 3704

GCTTGCTGAA ACTGGAAGTT ATTTATTTTT TAATGGCCCT TGAGAGTCAT GAACACATCA 3764

GCTAGCAACA GAAGTAACAA GAGTGATTCT TGCT 3798

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Leu Lys Pro Gln Pro Gln Pro Pro Ala Pro Ala Thr Gly Arg
 1 5 10 15

Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro Gly Ala Ala Pro Ala Ser
 20 25 30

Ala Ala Val Thr Ser Ala Ser Val Val Pro Ala Pro Ala Ala Pro Val
 35 40 45

Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly Arg Pro Gly Leu Gly Arg
 50 55 60

Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln Pro Thr Ile Ser Phe Asp
 65 70 75 80

Gly Ile Tyr Ala Asn Val Arg Met Val His Ile Leu Thr Ser Val Val
 85 90 95

Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly
 100 105 110

Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala
 115 120 125

His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile
 130 135 140

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Met Glu Ser Val Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe
 145 150 155 160
 Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg Asp Ala Phe Thr Asp Ser
 165 170 175
 Ala Leu Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu
 180 185 190
 Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser Glu Glu Leu Glu Leu Glu
 195 200 205
 Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn
 210 215 220
 Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser
 225 230 235 240
 Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg
 245 250 255
 Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln
 260 265 270
 Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu
 275 280 285
 Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly
 290 295 300
 Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
 305 310 315 320
 Glu Val Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly
 325 330 335
 Gln Pro Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser
 340 345 350
 Asp Phe Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly
 355 360 365
 Val Pro Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser
 370 375 380
 Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His
 385 390 395 400
 Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser
 405 410 415
 His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys
 420 425 430

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Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg
 435 440 445
 His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser
 450 455 460
 Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro
 465 470 475 480
 Pro Val Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val
 485 490 495
 Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro
 500 505 510
 Arg Gln Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser
 515 520 525
 Pro Gln Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro
 530 535 540
 Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr
 545 550 555 560
 Pro Ser Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn
 565 570 575
 Ser Pro Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro
 580 585 590
 Ser Phe Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu
 595 600 605
 His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg
 610 615 620
 Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys
 625 630 635 640
 Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Glu
 645 650 655
 Ala Ser Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Ser Asn
 660 665 670
 Cys Thr Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser
 675 680 685
 Met Leu Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln
 690 695 700
 Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg
 705 710 715 720

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Glu Glu Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn
 725 730 735
 Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro
 740 745 750
 Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser
 755 760 765
 Met Val Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys
 770 775 780
 Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln
 785 790 795 800
 Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys
 805 810 815
 Thr Tyr Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp
 820 825 830
 Gln His His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro
 835 840 845
 Pro Ile Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
 850 855 860
 Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
 865 870 875 880
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
 885 890 895
 Ala Arg Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser
 900 905 910
 Ser Ser Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr
 915 920 925
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
 930 935 940
 Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
 945 950 955 960
 Ala Ala Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
 965 970 975
 Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
 980 985 990
 Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
 995 1000 1005

009090-01100

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
 1010 1015 1020

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser
 1025 1030 1035 1040

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
 1045 1050 1055

Gln Pro Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala
 1060 1065 1070

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
 1075 1080 1085

Met Met Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala
 1090 1095 1100

Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro
 1105 1110 1115 1120

Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1125 1130 1135

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 Contain